



## SEQUENCE LISTING

<110> Human Genome Sciences, Inc.

<120> Albumin Fusion Proteins

<130> PF545PCT

<140> Unassigned

<141> 2001-04-12

<150> 60/229,358

<151> 2000-04-12

<150> 60/256,931

<151> 2000-12-21

<150> 60/199,384

<151> 2000-04-25

<160> 90

<170> PatentIn Ver. 2.1

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with non-cohesive ends.

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<223> invertase leader sequence

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<223> first 5 amino acids of mature human serum albumin

<400> 7

Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys  
1 5 10 15

Ile Ser Ala Asp Ala His Lys Ser  
20

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<400> 15

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gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag 96  
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln  
20 25 30  
cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144  
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
35 40 45  
ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192  
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
50 55 60  
tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt 240  
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
65 70 75 80  
cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct 288  
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
85 90 95  
gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336  
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
100 105 110  
ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat 384  
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
115 120 125  
gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga 432  
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg  
130 135 140

aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg	480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg	
145 150 155 160	
tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc	528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala	
165 170 175	
tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg	576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser	
180 185 190	
tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa	624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu	
195 200 205	
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc	672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro	
210 215 220	
aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa	720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys	
225 230 235 240	
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac	768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp	
245 250 255	
agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc	816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser	
260 265 270	
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac	864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His	
275 280 285	
tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca	912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser	
290 295 300	
tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct	960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala	
305 310 315 320	
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga	1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg	
325 330 335	
agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca	1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr	
340 345 350	

tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa	1104
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu	
355 360 365	
tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct	1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro	
370 375 380	
cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag	1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu	
385 390 395 400	
tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc	1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro	
405 410 415	
caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa	1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys	
420 425 430	
gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt	1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys	
435 440 445	
gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat	1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His	
450 455 460	
gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc	1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser	
465 470 475 480	
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca	1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr	
485 490 495	
tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat	1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp	
500 505 510	
ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca	1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala	
515 520 525	
ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg	1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu	
530 535 540	
aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag	1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys	



545		550		555		560	
gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt							1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val							
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gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag	1782
Ala Ala Ser Gln Ala Ala Leu Gly Leu	

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 <213> Homo Sapiens

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Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu	
	35
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys	
	50
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu	
	65
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro	
	85
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu	
	100
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His	
	115
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg	
	130
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg	
	145
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala	
	165
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser	

180					185					190					
Ser	Ala	Lys	Gln	Arg	Leu	Lys	Cys	Ala	Ser	Leu	Gln	Lys	Phe	Gly	Glu
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Arg	Ala	Phe	Lys	Ala	Trp	Ala	Val	Ala	Arg	Leu	Ser	Gln	Arg	Phe	Pro
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Lys	Ala	Glu	Phe	Ala	Glu	Val	Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	Lys
225					230					235					240
Val	His	Thr	Glu	Cys	Cys	His	Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp
				245					250					255	
Arg	Ala	Asp	Leu	Ala	Lys	Tyr	Ile	Cys	Glu	Asn	Gln	Asp	Ser	Ile	Ser
			260					265					270		
Ser	Lys	Leu	Lys	Glu	Cys	Cys	Glu	Lys	Pro	Leu	Leu	Glu	Lys	Ser	His
		275					280					285			
Cys	Ile	Ala	Glu	Val	Glu	Asn	Asp	Glu	Met	Pro	Ala	Asp	Leu	Pro	Ser
	290					295					300				
Leu	Ala	Ala	Asp	Phe	Val	Glu	Ser	Lys	Asp	Val	Cys	Lys	Asn	Tyr	Ala
305					310					315					320
Glu	Ala	Lys	Asp	Val	Phe	Leu	Gly	Met	Phe	Leu	Tyr	Glu	Tyr	Ala	Arg
				325					330					335	
Arg	His	Pro	Asp	Tyr	Ser	Val	Val	Leu	Leu	Leu	Arg	Leu	Ala	Lys	Thr
			340					345					350		
Tyr	Glu	Thr	Thr	Leu	Glu	Lys	Cys	Cys	Ala	Ala	Ala	Asp	Pro	His	Glu
		355					360					365			
Cys	Tyr	Ala	Lys	Val	Phe	Asp	Glu	Phe	Lys	Pro	Leu	Val	Glu	Glu	Pro
	370					375					380				
Gln	Asn	Leu	Ile	Lys	Gln	Asn	Cys	Glu	Leu	Phe	Glu	Gln	Leu	Gly	Glu
385					390					395					400
Tyr	Lys	Phe	Gln	Asn	Ala	Leu	Leu	Val	Arg	Tyr	Thr	Lys	Lys	Val	Pro
				405					410					415	
Gln	Val	Ser	Thr	Pro	Thr	Leu	Val	Glu	Val	Ser	Arg	Asn	Leu	Gly	Lys
			420					425					430		
Val	Gly	Ser	Lys	Cys	Cys	Lys	His	Pro	Glu	Ala	Lys	Arg	Met	Pro	Cys
		435					440					445			
Ala	Glu	Asp	Tyr	Leu	Ser	Val	Val	Leu	Asn	Gln	Leu	Cys	Val	Leu	His

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Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser		
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Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr		
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Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp		
	500	505 510
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala		
	515	520 525
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu		
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Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys		
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Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val		
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Ala Ala Ser Gln Ala Ala Leu Gly Leu		
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 site in pPPC0006

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site in pPPC0006

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 of the Therapeutic Protein  
  
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<223> reverse primer useful for generation of albumin fusion protein in which the albumin moiety is N-terminal of the Therapeutic Protein

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<223> forward primer useful for generation of albumin fusion protein in which the albumin moiety is c-terminal of the Therapeutic Protein

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Tyr Ser Arg Ser Leu Asp Lys Arg  
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 Ala  
  
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<220>  
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Thr Cys Cys Ala Gly Gly Cys  
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Ala Gly Gly Asn Ala His Ser Pro Leu Gly Val Pro Gly Gly Gly Leu  
35 40 45

Pro Glu His Thr Phe Asn Leu Lys Met Phe Leu Glu Asn Val Lys Val  
50 55 60

Asp Phe Leu Arg Ser Leu Asn Leu Ser Gly Val Pro Ser Gln Asp Lys  
65 70 75 80

Thr Arg Val Glu Pro Pro Gln Tyr Met Ile Asp Leu Tyr Asn Arg Tyr

85								90					95				
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Gln	Lys	His	Ile	Leu	Leu	Phe	Asn	Ile	Ser	Ile	Pro	Arg	His	Glu	Gln		
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Asp	Pro	Ser	His	Asp	Leu	Lys	Gly	Ser	Val	Val	Ile	Tyr	Asp	Val	Leu		
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Arg	Glu	Met	Ile	Ser	His	Glu	Gln	Glu	Ser	Val	Leu	Lys	Lys	Leu	Ser		
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Glu	Asp	Ile	Gly	Trp	Asp	Ser	Trp	Ile	Ile	Ala	Pro	Lys	Glu	Tyr	Glu		
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Ala	Tyr	Glu	Cys	Lys	Gly	Gly	Cys	Phe	Phe	Pro	Leu	Ala	Asp	Asp	Val		

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 Pro Thr Lys Val Gly Lys Ala Cys Cys Val Pro Thr Lys Leu Ser Pro  
 385                      390                      395                      400  
 Ile Ser Val Leu Tyr Lys Asp Asp Met Gly Val Pro Thr Leu Lys Tyr  
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 Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val Leu  
       1                      5                      10                      15  
 Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn Val Arg  
                     20                      25                      30  
 Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly Asp Trp Met  
                     35                      40                      45  
 Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln Asn Leu Gln Pro  
       50                      55                      60  
 Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp Leu Glu Val Asn Ile  
       65                      70                      75                      80  
 Ala Lys Val Asp Val Thr Glu Gln Pro Gly Leu Ser Gly Arg Phe Ile  
                     85                      90                      95  
 Ile Thr Ala Leu Pro Thr Ile Tyr His Cys Lys Asp Gly Glu Phe Arg  
                     100                      105                      110  
 Arg Tyr Gln Gly Pro Arg Thr Lys Lys Asp Phe Ile Asn Phe Ile Ser  
                     115                      120                      125  
 Asp Lys Glu Trp Lys Ser Ile Glu Pro Val Ser Ser Trp Phe Gly Pro  
       130                      135                      140  
 Gly Ser Val Leu Met Ser Ser Met Ser Ala Leu Phe Gln Leu Ser Met  
       145                      150                      155                      160  
 Trp Ile Arg Thr Cys His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro



<211> 346  
 <212> PRT  
 <213> Homo sapiens

<400> 77

Met	Asp	Pro	Ala	Arg	Lys	Ala	Gly	Ala	Gln	Ala	Met	Ile	Trp	Thr	Ala
1				5					10					15	
Gly	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Gly	Gly	Ala	Gln	Ala	Leu	Glu
			20					25					30		
Cys	Tyr	Ser	Cys	Val	Gln	Lys	Ala	Asp	Asp	Gly	Cys	Ser	Pro	Asn	Lys
		35					40					45			
Met	Lys	Thr	Val	Lys	Cys	Ala	Pro	Gly	Val	Asp	Val	Cys	Thr	Glu	Ala
	50					55					60				
Val	Gly	Ala	Val	Glu	Thr	Ile	His	Gly	Gln	Phe	Ser	Leu	Ala	Val	Arg
65					70					75					80
Gly	Cys	Gly	Ser	Gly	Leu	Pro	Gly	Lys	Asn	Asp	Arg	Gly	Leu	Asp	Leu
				85					90					95	
His	Gly	Leu	Leu	Ala	Phe	Ile	Gln	Leu	Gln	Gln	Cys	Ala	Gln	Asp	Arg
			100					105					110		
Cys	Asn	Ala	Lys	Leu	Asn	Leu	Thr	Ser	Arg	Ala	Leu	Asp	Pro	Ala	Gly
		115					120					125			
Asn	Glu	Ser	Ala	Tyr	Pro	Pro	Asn	Gly	Val	Glu	Cys	Tyr	Ser	Cys	Val
	130					135					140				
Gly	Leu	Ser	Arg	Glu	Ala	Cys	Gln	Gly	Thr	Ser	Pro	Pro	Val	Val	Ser
145					150					155					160
Cys	Tyr	Asn	Ala	Ser	Asp	His	Val	Tyr	Lys	Gly	Cys	Phe	Asp	Gly	Asn
				165					170					175	
Val	Thr	Leu	Thr	Ala	Ala	Asn	Val	Thr	Val	Ser	Leu	Pro	Val	Arg	Gly
			180					185					190		
Cys	Val	Gln	Asp	Glu	Phe	Cys	Thr	Arg	Asp	Gly	Val	Thr	Gly	Pro	Gly
		195					200					205			
Phe	Thr	Leu	Ser	Gly	Ser	Cys	Cys	Gln	Gly	Ser	Arg	Cys	Asn	Ser	Asp
	210					215					220				
Leu	Arg	Asn	Lys	Thr	Tyr	Phe	Ser	Pro	Arg	Ile	Pro	Pro	Leu	Val	Arg
225					230					235					240
Leu	Pro	Pro	Pro	Glu	Pro	Thr	Thr	Val	Ala	Ser	Thr	Thr	Ser	Val	Thr





130		135		140
Thr 145	Ala Gly Pro	Asn Pro 150	Thr Leu Gly Arg Pro 155	Leu Ser Pro Lys Pro 160
Ser	Ser Pro Gly	Ser 165 Val Leu Ala Arg Pro 170	Ser Val Ile Cys His 175	Thr
Thr	Val Thr 180	Ala Leu Lys Asp Val Pro Phe 185	Ser Leu Cys Gln Ser 190	Val
Gly	Val Gly 195	Gln Asn Thr Asp Ile Gln Gln 200	Ile Ala Ala Lys Asn Phe 205	
Thr	Asp Thr 210	Ser Leu Met Tyr Pro Glu Asp Thr 215	Cys Lys Ser Gly Pro 220	
Ser 225	Thr Asn Thr	Gln Ser 230 Gly Leu Phe Asn Thr 235	Pro Pro Pro Thr	Pro 240
Pro	Asp Leu Asn 245	Gln Asp Phe Ser Gly Phe Gln Leu Leu Val Asp 255	Val	
Ala	Leu Lys Arg 260	Ala Ala Glu Met Glu Leu Gln Ala Lys Leu Thr 270	Ala	

<210> 79  
 <211> 167  
 <212> PRT  
 <213> Homo sapiens

<400> 79

Met 1	Leu Thr Val	Ala 5	Leu Leu Ala Leu 10	Cys Ala Ser Ala 15	Ser Gly
Asn	Ala Ile 20	Gln Ala Arg Ser Ser 25	Tyr Ser Gly Glu Tyr 30	Gly Gly	
Gly	Gly Gly 35	Lys Arg Phe Ser His 40	Ser Gly Asn Gln Leu 45	Asp Gly Pro	
Ile 50	Thr Ala Leu Arg Val Arg 55	Val Asn Thr Tyr Tyr 60	Ile Val Gly Leu		
Gln 65	Val Arg Tyr Gly Lys 70	Val Trp Ser Asp Tyr 75	Val Gly Gly Arg Asn 80		
Gly	Asp Leu Glu Glu 85	Ile Phe Leu His Pro Gly 90	Glu Ser Val Ile Gln 95		
Val	Ser Gly Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr				

100	105	110
Asp Lys Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe		
115	120	125
Asn Ala Val Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly		
130	135	140
Arg Ser Gly Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr		
145	150	155
		160
Pro Thr Ser Cys Ser Arg Cys		
165		

<210> 80  
 <211> 22  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> (22)  
 <223> Xaa equals stop translation

<400> 80

Met Leu Ala Ala Leu Ala Cys Ser Trp Arg Leu Leu Ser Leu Gly Ala
1 5 10 15
His Ser Gly Arg Ala Xaa
20

<210> 81  
 <211> 733  
 <212> DNA  
 <213> Homo sapiens

<400> 81  
 gggatccgga gcccaaattct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60  
 aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 120  
 tctcccggac tcctgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180  
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240  
 aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300  
 ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg 360

agaaaacccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc	420
catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct	480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga	540
ccacgcctcc cgtgctggac tccgacggct ctttcttct ctacagcaag ctcaccgtgg	600
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc	660
acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc	720
gactctagag gat	733

<210> 82  
 <211> 5  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_structure  
 <223> membrane proximal motif of class 1 cytokine receptors

<220>  
 <221> misc\_feature  
 <222> (3)  
 <223> Xaa equals any

<400> 82  
 Trp Ser Xaa Trp Ser  
 1 5

<210> 83  
 <211> 86  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <223> forward primer useful for generation of a synthetic gamma  
 activation site (GAS) containing promoter element

<400> 83	
ggcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc	60
cccgaaatat ctgccatctc aattag	86

<210> 84  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <223> reverse primer useful for generation of a synthetic gamma  
 activation site (GAS) containing promoter element

<400> 84  
 gcggcaagct ttttgcaaag cctaggc 27

<210> 85  
 <211> 271  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> misc\_feature  
 <223> Synthetic GAS-SV40 promoter sequence

<400> 85  
 ctcgagatTTT ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60  
 aaatatctgc catctcaatt agtcagcaac catagtccccg cccctaactc cgcccatccc 120  
 gccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180  
 ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240  
 ttttgagggc ctaggctttt gcaaaaagct t 271

<210> 86  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <223> primer useful for generation of a EGR/SEAP reporter construct

<400> 86  
 gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 87  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <223> primer useful for generation of a EGR/SEAP reporter construct  
  
 <400> 87  
 gcgaagcttc gcgactcccc ggatccgcct c 31  
  
 <210> 88  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <221> misc\_binding  
 <223> NF-KB binding site  
  
 <400> 88  
 ggggactttc cc 12  
  
 <210> 89  
 <211> 73  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <221> primer\_bind  
 <223> forward primer useful for generation of a vector containing the  
 NF-KB promoter element  
  
 <400> 89  
 gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatcctg 60  
 ccatctcaat tag 73  
  
 <210> 90  
 <211> 256  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <221> misc\_feature  
 <223> Synthetic NF-KB/SV40 promoter  
  
 <400> 90  
 ctcgagggga ctttcccggg gactttccgg ggactttccg ggactttcca tctgccatct 60  
 caattagtca gcaaccatag tcccgccct aactccgccc atcccgcccc taactccgcc 120  
 cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180

ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg	240
cttttgcaaa aagctt	256